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SCORE
STDEV
Sequence Name
                                                                                                Number of residues:
Number of sequences searched:
Number of scores above cutoff:
                                                                                                                                                                                                                                      Gap penalty
Gap size penalty
Cutoff score
                                                                                                                                                                                                                                                                                                                                                                  SECZEGÓES
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                                                       The scores below are sorted by initial score. Significance is calculated based on initial s
                                                                                                                                                                                                                                                                    Similarity matrix Mismatch penalty
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Results file us2.res made by schreib
                                  100% identical sequence to the
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    Description
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291
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0.05
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                                                                                                                                                                                                                                                                                                    PARAMETERS
                                   query sequence was found:
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Joining penalty
Window size
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204
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                                                        score
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                                                                                                                                                                       Standard Deviation 125.16
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 Length Score Score Sig. Frame
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32
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Gaps
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US-08-809-572-4 Sequence 4, Application US/08609572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The list of other best scores is:
                                                                                                                                                                                                                                                                          TELEPHONE: (617) 498-82
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08609572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Wood, Clive
APPLICANT: Wood, Clive
TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,572
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: GI5268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 6, Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                    LENGTH: 380 amino TYPE: amino acid TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
ZIP: 02140
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Donaldson, Debra
Fitz, Lori
Neben, Tamlyn
Whitters, Matthew
Wood, Clive
                                                                                                                                                                                                                                                               380 amino acids
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                                                                                                                                                                                                                                                                                                        (617) 498-8224
(617) 876-5851
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100% Matches
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Mismatches
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CVYYNWQYLLCSWKPGIGVLLDINYNLFYWYEGLDHALQCVDYIKADGQNIGCRFPYLEASDYKDFYICVNG

180

190

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Sequence 2, Application US/08609572
Pattent No. 5710023
GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Donaldson, Debra
APPLICANT: Neben, Tamlyn
APPLICANT: Neben, Tamlyn
APPLICANT: Whitters, Matthew
APPLICANT: Wood, Clive
TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                 Initial Score
Residue Identity
Gaps
                                                                                                                                                                              REFERENCE/DOCKET NUMBER: GI5268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEPAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/609,572
FILING DATE:
CLASSIFICATION: 530
CCLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-815-773-2 (1-380)
US-08-609-572-2 Sequence 2, Application US/08609572
X 10 20 30 40 50 60 70 MAFVCLAIGCLYTFLISTTFGCTSSSDTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLDHFKBCTVEYELK
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LLLRKPNTYPKMIPEFFCDT
LLLRKPNTYPKMIPEFFCDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSENKPIRSSYETFOLONIVKPLPPVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTTLVTATV SSENKPIRSSYETFOLONIVKPLPPVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTTLVTATV SSENKPIRSSYETFOLONIVKPLPPVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTTLVTATV 220 230 240 250 260
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CITY: Cambr
STATE: MA
COUNTRY: US
ZIP: 02140
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                                                                                          Optimized Score 220
Matches 226
Conservative Substitutions
                                                                                                              Significance
Mismatches
                                                                                      -0.70
139
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60 370 x
TGLLLRKPNTYPKMIPE-----FFCDT
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                                                                                                                                                                                                                                                                                              MAFV--HIRCLCFILLCTITG----YSLEIKVNPPQDFEILDPGLLGYLYLQWKPPVVIEKFKGCTLEYELR
X 10 20 30 40 50 60
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